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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/555,981C

DATE: 04/23/2002
TIME: 07:57:28

Input Set : A:\5008.ST25.txt

Output Set: N:\CRF3\04232002\I555981C.raw

3 <110> APPLICANT: Lead B.V.
4 NOTEBORN, Mathieu Hubertus Maria
5 DAMEN-VAN OORSCHOT, Astrid Adriana Anna Maria
7 <120> TITLE OF INVENTION: MOLECULES INTERACTING WITH APOPTIN
9 <130> FILE REFERENCE: 2906-5008
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/555,981C
12 <141> CURRENT FILING DATE: 2000-06-26
14 <160> NUMBER OF SEQ ID NOS: 16
16 <170> SOFTWARE: PatentIn version 3.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 17
20 <212> TYPE: DNA
21 <213> ORGANISM: Artificial Sequence
23 <220> FEATURE:
24 <221> NAME/KEY: misc_feature
25 <223> OTHER INFORMATION: Description of Artifical Sequence: pACT-specific sequenceing
prim
26 e
29 <400> SEQUENCE: 1
30 taccactaca atggatg 17
33 <210> SEQ ID NO: 2
34 <211> LENGTH: 15
35 <212> TYPE: PRT
36 <213> ORGANISM: Artificial Sequence
38 <220> FEATURE:
39 <221> NAME/KEY: misc_feature
40 <223> OTHER INFORMATION: Description of Artificial Sequence; Hou/Nmi-like protein
putative
41 immunogenic peptid
44 <400> SEQUENCE: 2
46 Arg Asn Gly Gly Gly Glu Val Asp Arg Val Asp Tyr Asp Arg Gln
47 1 5 10 15
49 <210> SEQ ID NO: 3
50 <211> LENGTH: 16
51 <212> TYPE: PRT
52 <213> ORGANISM: Artificial Sequence
54 <220> FEATURE:
55 <221> NAME/KEY: misc_feature
56 <223> OTHER INFORMATION: Description of Artificial Sequence: IEP35-like protein
putative i
57 mmunogenic peptid
60 <400> SEQUENCE: 3
62 Cys Gln Leu Arg Lys Glu Leu Gly Asp Ser Pro Lys Asp Lys Val Pro
63 1 5 10 15

65 <210> SEQ ID NO: 4
66 <211> LENGTH: 658

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```

67 <212> TYPE: DNA
68 <213> ORGANISM: Homo sapien
70 <220> FEATURE:
71 <221> NAME/KEY: misc_feature
72 <223> OTHER INFORMATION: N is an undefined base
75 <400> SEQUENCE: 4
76 gggggatcat ggaagctgat aaagatgaca cacaacaaat tcttaaggag cattcgccag      60
77 atgaatttat aaaagatgaa caaaataagg gactaattga tgaaattaca aagaaaaata      120
78 ttcaactaaa gaaggagatc caaaagcttg aaacggagtt acaagaggct accaaagaat      180
79 tccagattaa agaggatatt cctgaaacaa agatgaaatt cttatcagtt gaaactcctg      240
80 agaatgacag ccagttgtca aatatctcct gttcgtttca agtgagctcg aaagtctcct      300
81 atgagatata aaaaggacaa gcacttatca cctttgaaaa agaagaagtt gctcaaaatg      360
82 tggtaagcat gagtaaacat catgtacaga taaaagatgt aaatctggag gttacggcca      420
83 agccagttcc attaaattca ggagtcagat tccagggttta tgtagaagtt tctaaaatga      480
84 aaatcaatgt tactgaaatt cctgacacat tgcgtgaaga tcaaatgaga gacaaactag      540
W--> 94 agctgagctt ttcaaagtcc cgaaatggga ggcgggagang tggaccgcgt gggactatga      600
W--> 96 cagacagtcg gggagtgcag tcatcacgtt tggnggagat tgggagtggc tgacannn      658
99 <210> SEQ ID NO: 5
100 <211> LENGTH: 719
101 <212> TYPE: DNA
102 <213> ORGANISM: Homo sapien
104 <220> FEATURE:
105 <221> NAME/KEY: misc_feature
106 <223> OTHER INFORMATION: N is an undefined base
109 <400> SEQUENCE: 5
110 cggaggttaca agaggctacc aaagaattcc agattaaaga ggatattcct gaaacaaaga      60
W--> 112 tgaaattctt atcagttgaa actcctgana atgacagcca gttgtcaa atctcctgtt      120
114 cgtttcaagg tgagctcgaa agttccttat gagatacaaa aaggacaatg cacttatcac      180
W--> 116 ctttgaaaaa ggaagaagtt gctcaaaatg tngntaangc atgagtaa atcatgtaca      240
118 gataataaga tgtaaactctg gaggttacgg ccaaagccaa gttccattaa tattcaagga      300
W--> 120 gtcangattc cagngtttat gctagaangt ttctaaaaat ganaatcaat gggtactgga      360
W--> 122 aattcctgga cacattgcgn tgaaagatca agatgacgaa gacaaactaa gaagctgagc      420
W--> 124 ttttcaaaag tcccgaanaa tggaagagcg gtagagggtg gnaccgcgtg nganctatga      480
W--> 126 caagacaagn ccggggaagn tgcagtccat cacgtttgtn ngaagattgg angtnngctg      540
W--> 128 accaangaat tttgaaaaag gagangaatt acccctcttt angagtaana tcaaaacctt      600
W--> 130 gccataanaa gtttactggt ttncgccatt acacagnant tacannttga ncaanantan      660
W--> 132 ncaggataat ttncagggga anaatctnaa gnatggcaag ntgacttctg gacaanggt      719
135 <210> SEQ ID NO: 6
136 <211> LENGTH: 220
137 <212> TYPE: PRT
138 <213> ORGANISM: Homo sapiens
140 <400> SEQUENCE: 6
142 His Glu Gly Arg Gly Ile Met Glu Ala Asp Lys Asp Asp Thr Gln Gln
143 1 5 10 15
145 Ile Leu Lys Glu His Ser Pro Asp Glu Phe Ile Lys Asp Glu Gln Asn
146 20 25 30
148 Lys Gly Leu Ile Asp Glu Ile Thr Lys Lys Asn Ile Gln Leu Lys Lys
149 35 40 45
151 Glu Ile Gln Lys Leu Glu Thr Glu Leu Gln Glu Ala Thr Lys Glu Phe

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152      50      55      60
154 Gln Ile Lys Glu Asp Ile Pro Glu Thr Lys Met Lys Phe Leu Ser Val
155 65      70      75      80
157 Glu Thr Pro Glu Asn Asp Ser Gln Leu Ser Asp Ile Ser Cys Ser Phe
158      85      90      95
160 Gln Val Ser Ser Lys Val Pro Thr Glu Ile Gln Lys Gly Gln Ala Leu
161      100     105     110
163 Ile Thr Phe Glu Lys Glu Glu Val Ala Gln Asn Val Val Ser Met Ser
164      115     120     125
166 Lys His His Val Gln Ile Lys Asp Val Asn Leu Glu Val Thr Ala Lys
167      130     135     140
169 Pro Val Pro Leu Asn Ser Gly Val Arg Phe Gln Val Thr Val Glu Val
170 145     150     155     160
172 Ser Lys Met Lys Ile Asn Val Thr Glu Ile Pro Asp Thr Leu Arg Glu
173      165     170     175
175 Asp Gln Met Arg Arg Lys Leu Glu Leu Ser Phe Ser Lys Ser Arg Asn
176      180     185     190
178 Gly Arg Arg Arg Cys Gly Pro Arg Gly Thr Met Thr Asp Ser Pro Gly
179      195     200     205
181 Val Gln Ser Ser Arg Leu Val Glu Ile Gly Ser Gly
182      210     215     220
184 <210> SEQ ID NO: 7
185 <211> LENGTH: 307
186 <212> TYPE: PRT
187 <213> ORGANISM: Homo sapiens
189 <400> SEQUENCE: 7
191 Met Glu Ala Asp Lys Asp Asp Thr Gln Gln Ile Leu Lys Glu His Ser
192 1      5      10      15
194 Pro Asp Glu Phe Ile Lys Asp Glu Gln Asn Lys Gly Leu Ile Asp Glu
195      20      25      30
197 Ile Thr Lys Lys Asn Ile Gln Leu Lys Lys Glu Ile Gln Lys Leu Glu
198      35      40      45
200 Thr Glu Leu Gln Glu Ala Thr Lys Glu Phe Gln Ile Lys Glu Asp Ile
201      50      55      60
203 Pro Glu Thr Lys Met Lys Phe Leu Ser Val Glu Thr Pro Glu Asn Asp
204 65      70      75      80
206 Ser Gln Leu Ser Asn Ile Ser Cys Ser Phe Gln Val Ser Ser Lys Val
207      85      90      95
209 Pro Tyr Glu Ile Gln Lys Gly Gln Ala Leu Ile Thr Phe Glu Lys Glu
210      100     105     110
212 Glu Val Ala Gln Asn Val Val Ser Met Ser Lys His His Val Gln Ile
213      115     120     125
215 Lys Asp Val Asn Leu Glu Val Thr Ala Lys Pro Val Pro Leu Asn Ser
216      130     135     140
218 Gly Val Arg Phe Gln Val Thr Val Glu Val Ser Lys Met Lys Ile Asn
219 145     150     155     160
221 Val Thr Glu Ile Pro Asp Thr Leu Lys Glu Asp Gln Met Arg Asp Lys
222      165     170     175
224 Leu Glu Leu Ser Phe Ser Lys Phe Arg Asn Gly Gly Gly Glu Val Asp

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```

225          180          185          190
227 Arg Val Asp Tyr Asp Arg Gln Ser Gly Ser Ala Val Ile Thr Phe Val
228          195          200          205
230 Glu Ile Gly Val Ala Asp Lys Ile Leu Lys Lys Lys Glu Tyr Pro Leu
231          210          215          220
233 Tyr Ile Asn Gln Thr Cys His Arg Val Thr Val Ser Pro Tyr Thr Glu
234 225          230          235          240
236 Ile His Leu Lys Lys Tyr Gln Ile Phe Ser Gly Thr Ser Lys Arg Thr
237          245          250          255
239 Val Leu Leu Thr Gly Met Glu Gly Ile Gln Met Asp Glu Glu Ile Val
240          260          265          270
242 Glu Asp Leu Ile Asn Ile His Phe Gln Arg Ala Lys Asn Gly Gly Gly
243          275          280          285
245 Glu Val Asp Val Val Lys Cys Ser Leu Gly Gln Pro His Ile Ala Tyr
246          290          295          300
248 Phe Glu Glu
249 305
251 <210> SEQ ID NO: 8
252 <211> LENGTH: 659
253 <212> TYPE: DNA
254 <213> ORGANISM: Homo sapiens
256 <220> FEATURE:
257 <221> NAME/KEY: misc_feature
258 <223> OTHER INFORMATION: N is an undefined base
261 <400> SEQUENCE: 8
262 agcaggtgct gcaacaaaag gagcacacga tcaacatgga ggagtgccgg ctgcgggtgc      60
264 aggtccagcc cttggagctg cccatgggtca ccaccatcca ggtgtccagc cagttgagtg      120
266 gccggagggt gttggtcact ggatttcctg ccagcctcag gctgagtgag gaggagctgc      180
W--> 268 tggacaanct anagatcttc tttggcaaga ctaggaacgg aggtggcnat gtggacnttc      240
W--> 270 ggganctact gccagggant gtcattgctg ggtttgctag ggatggagtg gtcancgtc      300
W--> 272 tgtgccaaat cggccatttc acagtgccac tgggtgggca gcangtcct ctgagagtct      360
W--> 274 ctccgtatgt gaatggggan atccagangg ctganatcag gtcncagcca ntccccgct      420
276 cggtagctggt gctcaacatt cctgatatct tggatggccc ggagctgcat gacgtcctg      480
W--> 278 anatccactt ccagaanccc acccgcgggg gcggagatgt aagacgccct gacagtcgta      540
W--> 280 cccaaggac aacagggcct aacagtcttc acctcctgaa tcaaggctan gggcctcccc      600
W--> 282 cttctcatcc tccccacccc ccccgccaaa ggtttctaan actgggcctg ggctttntg      659
285 <210> SEQ ID NO: 9
286 <211> LENGTH: 630
287 <212> TYPE: DNA
288 <213> ORGANISM: Homo sapiens
290 <220> FEATURE:
291 <221> NAME/KEY: misc_feature
292 <223> OTHER INFORMATION: N is an undefined base
295 <400> SEQUENCE: 9
296 ccaaagtggc tgagcaggtg ctgcaacaaa aggagcacac gatcaacatg gaggagtgcc      60
298 ggctgcgggt gcaggtccag cccttgagc tgcccatggt caccaccatc caggtgtcca      120
300 gccagttgag tggccggagg gtgttggtca ctggatttcc tgccagcctc aggctgagtg      180
302 aggaggagct gctggacaag ctagagatct tctttggcaa gactaggaac ggaggtggcg      240
304 atgtggacgt tcgggagcta ctgccaggga gtgtcatgct ggggtttgct agggatggag      300

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W--> 306 tggtcagcg tctgtgcaa atcggccaag ttcacagtgc cactgggtgg gcancaagtc 360
W--> 308 cctctgagag tctctccgta tgtgaatggg gagatccaga aggctgagat caggctcgcan 420
W--> 310 ccagttcccc nctcgggtact ggggtgctcaa cattcctgat atcttggatt ggcccggagc 480
W--> 312 tgcatacgt cctgganac aacttcanaa gcccaccgc cggggcngng aggtanaagg 540
W--> 314 cctgacatcn ttaccccaaa ggacagcatg gncctaacag tcctcacctc cnaatcangc 600
W--> 316 tnnggggctn cccttctanc ntcccaactg 630
319 <210> SEQ ID NO: 10
320 <211> LENGTH: 631
321 <212> TYPE: DNA
322 <213> ORGANISM: Homo sapiens
324 <220> FEATURE:
325 <221> NAME/KEY: misc_feature
326 <223> OTHER INFORMATION: N is an undefined base
329 <400> SEQUENCE: 10
330 ggatccactg ccctctgctt gggggtcttg ctctgatcac ctttgatgac cccaaagtgg 60
332 ctgagcaggt gctgcaacaa aaggagcaca cgatcaacat ggaggagtgc cggctgcggg 120
334 tgcaggtcca gcccttgag ctgcccattg tcaccaccat ccaggtgatg gtgtccagcc 180
W--> 336 anttgagtgg ccggagggtg ttggtcactg gatttcctgc cagcctcagg ctgantgagg 240
W--> 338 aggagctgct ggacaagcta tgagatcttc tttggcaana ctangaacgg angtggcgat 300
340 gtggacgttc gggagctact gccaggaggt gtcagtctgg ggtttctac ggatggagtg 360
342 gctcagcgtc tgtgccaat cggccagttc acaagtgcc ctgggtgggc agcaagtccc 420
W--> 344 tctgagagtc tctccgatg tgantggnga gatcagaatg ctganattaa gtcgcatcca 480
W--> 346 attcctcgtc cnggtactgg tgctcannat cctganatct tggattggcc ccngantnca 540
W--> 348 tganatctgg nagattcaat tncanaagtc canccnncng ngncgggaag tanangcccc 600
W--> 350 ananttcntn ncntanggnc agcanngcct g 631
353 <210> SEQ ID NO: 11
354 <211> LENGTH: 138
355 <212> TYPE: PRT
356 <213> ORGANISM: Homo sapiens
358 <400> SEQUENCE: 11
360 His Glu Gly Pro Lys Val Ala Glu Gln Val Leu Gln Gln Lys Glu His
361 1 5 10 15
363 Thr Ile Asn Met Glu Glu Cys Arg Leu Arg Val Gln Val Gln Pro Leu
364 20 25 30
366 Glu Leu Pro Met Val Thr Thr Ile Gln Val Ser Ser Gln Leu Ser Gly
367 35 40 45
369 Arg Arg Val Leu Val Thr Gly Phe Pro Ala Ser Leu Arg Leu Ser Glu
370 50 55 60
372 Glu Glu Leu Leu Asp Lys Leu Glu Ile Phe Phe Gly Lys Thr Arg Asn
373 65 70 75 80
375 Gly Gly Gly Asp Val Asp Val Arg Glu Leu Leu Pro Gly Ser Val Met
376 85 90 95
378 Leu Gly Phe Ala Arg Asp Gly Val Ala Gln Arg Leu Cys Gln Ile Gly
379 100 105 110
381 Gln Val His Ser Ala Thr Gly Trp Ala Ser Ser Pro Ser Glu Ser Leu
382 115 120 125
384 Ser Val Cys Glu Trp Gly Asp Pro Glu Gly
385 130 135
387 <210> SEQ ID NO: 12

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VARIABLE LOCATION SUMMARY

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Use of n's or Xaa's(NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:4; N Pos. 579,634,656,657,658

Seq#:5; N Pos. 89,213,218,305,314,328,343,380,439,462,471,474,490,500,520

Seq#:5; N Pos. 521,532,535,546,565,582,589,608,614,624,637,639,645,646,651

Seq#:5; N Pos. 655,657,660,661,673,682,688,692,701,716

Seq#:8; N Pos. 188,192,228,237,245,259,296,344,380,388,395,404,411,482,497

Seq#:8; N Pos. 590,640,657

Seq#:9; N Pos. 354,420,431,486,497,508,527,529,536,550,572,592,598,602,603

Seq#:9; N Pos. 610,619,621

Seq#:10; N Pos. 182,235,279,284,292,444,448,465,492,507,508,516,533,536,538

Seq#:10; N Pos. 544,551,562,565,573,576,577,579,581,583,593,595,602,604,608

Seq#:10; N Pos. 610,611,613,616,619,625,626

Seq#:13; Xaa Pos. 64,82,96,97,100,149,150,155,163,168,170,176,177,179,185

Seq#:13; Xaa Pos. 186,189,190,191,192,195,196,198,199,201,202,203,204,206

Seq#:16; Xaa Pos. 137,146,173,177,179,197,202,205,213

VERIFICATION SUMMARY

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Input Set : A:\5008.ST25.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:94 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
 L:94 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:540
 L:96 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
 L:96 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:600
 L:112 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
 L:112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:60
 L:116 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
 L:116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:180
 L:120 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
 L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:300
 L:122 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
 L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:360
 L:124 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
 L:124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:420
 L:126 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
 L:126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:480
 L:128 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
 L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:540
 L:130 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
 L:130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:600
 L:132 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
 L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:660
 L:268 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
 L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:1
 L:270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
 L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:2
 L:272 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
 L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:300
 L:274 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
 L:274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:360
 L:278 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
 L:278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after po
 L:280 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
 L:280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:40
 L:282 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
 L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:600
 L:306 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
 L:306 M:341 W: (46) "n" or "Xaa" used for SEQ ID#:9 af
 L:308 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
 L:308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:420
 L:310 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
 L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:420
 L:312 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
 L:312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:480
 L:314 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
 L:314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:540
 L:316 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9

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L:316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:600
L:336 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:180
L:338 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:338 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:240
L:344 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:344 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:420
L:346 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:480
L:348 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:540
L:350 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:350 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:600
L:469 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:469 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:48
L:475 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:475 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:80
L:478 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:478 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:96
L:487 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:144
L:490 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:160
L:493 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:176
L:496 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:496 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:192
L:714 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:714 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:128
L:717 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:717 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:144
L:720 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:720 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:160
L:723 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:723 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:176
L:726 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:192
L:729 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:208